



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 21, 2004, 09:55:38 (without alignments)

Search time 24 Seconds  
1489.392 Million cell updates/sec

Title: US-09-701-747a-2

Perfect score: 2892

Sequence: 1 MPIEIVCKIKFAEEDAKPKE.....LPNHHHPPGPPGSLFENFAC 539

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/pctodata/1/iaa/5b\_COMB.pep:\*

2: /cgn2\_6/pctodata/1/iaa/5b\_COMB.pep:\*

3: /cgn2\_6/pctodata/1/iaa/6b\_COMB.pep:\*

4: /cgn2\_6/pctodata/1/iaa/6b\_COMB.pep:\*

5: /cgn2\_6/pctodata/1/iaa/pcutus\_COMB.pep:\*

6: /cgn2\_6/pctodata/1/iaa/packfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Match length DB ID Description

Result No.	Score	Query Match	length	DB ID	Description
1	2814	97.3	539	4	US-09-518-959-9
2	2811	97.2	539	4	US-09-518-959-9
3	1323	45.7	559	3	US-09-360-197-8
4	1275	44.1	526	3	US-09-360-197-2
5	1249	43.2	514	3	US-09-360-197-4
6	1198	41.4	533	3	US-09-360-197-10
7	1179	40.8	512	2	US-09-360-197-2
8	1179	40.8	512	3	US-09-360-197-5
9	1165	40.3	531	3	US-09-360-197-14
10	1132	39.5	563	3	US-09-360-197-12
11	413	41.3	702	4	US-09-917-254-94
12	409	14.2	564	3	US-09-360-197-16
13	409	14.1	698	1	US-08-376-362A-20
14	408	14.1	625	3	US-09-197-15
15	350	12.1	753	3	US-07-861-458C-98
16	347	12.0	493	6	5196333-4
17	330	11.4	755	3	US-07-861-458C-99
18	317	11.0	520	3	US-07-861-458C-100
19	225	7.8	294	5	5196333-2
20	408	4.7	97	6	5196333-9
21	122	4.2	173	6	5196333-6
22	116	4.0	67	6	5196333-10
23	113	3.9	159	4	US-09-538-092-887
24	110	3.8	1495	4	US-08-522-726B-1
25	110	3.8	1495	4	US-09-337-384-1
26	105	3.6	830	4	US-09-562-737-3
27	105	3.6	4545	2	US-08-804-227C-14

#### ALIGNMENTS

RESULT 1  
US-09-518-959-9  
Sequence 9, Application US/09518959  
Patent No. 6549270  
GENERAL INFORMATION:  
APPLICANT: Eriander, Mark G  
APPLICANT: Huver, Rene  
APPLICANT: Pyati, Jayashree  
TITLE OF INVENTION: DNA encoding human acid-sensing ion  
TITLE OF INVENTION: channel Bnac4 (ASIC4)  
FILE REFERENCE: ORT-1197  
CURRENT APPLICATION NUMBER: US/09/518, 959  
CURRENT FILING DATE: 2000-03-03  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 9  
LENGTH: 539  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 97.3%; Score 2814; DB 4; Length 539;  
Best Local Similarity 97.0%; Pred. No. 2,3e-24;  
Matches 523; Conservative 6; Mismatches 10; Indels 0; Gaps 0;  
OQ  
1 MPIEIVCKIKFAEEDAKPKE.....LPNHHHPPGPPGSLFENFAC 539  
1 MPIEIVCKIKFAEEDAKPKE.....LPNHHHPPGPPGSLFENFAC 539  
Db  
61 GPHGLRRTWALALTSLAFYQASILARGVLYTRPHVAMPAAPPAVGAVPTVNI 120  
61 GPHGLRRTWALALTSLAFYQASILARGVLYTRPHVAMPAAPPAVGAVPTVNI 120  
QY  
121 NRFRHSAISDADIFHLANLTGLPKDRGHRAGLRYRPEPDMDILNRTGHQALDMJSC 180  
121 NRFRHSAISDADIFHLANLTGLPKDRGHRAGLRYRPEPDMDILNRTGHQALDMJSC 180  
Db  
121 NRFRHSAISDADIFHLANLTGLPKDRGHRAGLRYRPEPDMDILNRTGHQALDMJSC 180  
121 NRFRHSAISDADIFHLANLTGLPKDRGHRAGLRYRPEPDMDILNRTGHQALDMJSC 180  
QY  
181 NFSCHHCCASNFSYVTTGCKTYNADPOSSLSPRAGMGSLEIMDIOBRYLPWR 240  
181 NFSCHHCCASNFSYVTTGCKTYNADPOSSLSPRAGMGSLEIMDIOBRYLPWR 240  
Db  
301 KLRPELQCGYSAYSVSACRLCRCEKEAVQRCHCRMVAVNGNTICPPNIYICADHTDS 360  
301 KLRPELQCGYSAYSVSACRLCRCEKEAVQRCHCRMVAVNGNTICPPNIYICADHTDS 360  
QY  
241 ENTSFSGIRQIHSQEPYTHQGVSQGQFQPTVSCQBRQTLQPGWNCLES 300  
241 ENTSFSGIRQIHSQEPYTHQGVSQGQFQPTVSCQBRQTLQPGWNCLES 300  
Db  
301 KLRPELQCGYSAYSVSACRLCRCEKEAVQRCHCRMVAVNGNTICPPNIYICADHTDS 360  
301 KLRPELQCGYSAYSVSACRLCRCEKEAVQRCHCRMVAVNGNTICPPNIYICADHTDS 360  
QY  
301 KLRPELQCGYSAYSVSACRLCRCEKEAVQRCHCRMVAVNGNTICPPNIYICADHTDS 360  
301 KLRPELQCGYSAYSVSACRLCRCEKEAVQRCHCRMVAVNGNTICPPNIYICADHTDS 360

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OM protein - protein search, using SW model

Run on: December 21, 2004, 07:58:43 ; Search time 79 Seconds

Post-processing: Maximum Match 0% ; 3925.657 Million cell updates/sec

Title: US-09-701-747a-2

Perfect score: 2892 ; 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539

Scoring table: BLOSUM62 ; Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0% ; Listing first 45 summaries

Database : UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2889	99.9	539	2	Q9QV9	Q9QV9	PRELIMINARY; PRT; 539 AA.
2	2883	99.7	539	2	Q0JHS6	Q9QV9;	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
3	2855	99.1	539	2	Q7TN7	Q9QV9;	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
4	2811	97.2	539	2	Q9NQ4	Q9NQ4	DB SPASIC protein.
5	2787	96.4	524	2	Q80XK4	Q80XK4	GN Name=Spasic;
6	2680	92.7	647	2	Q7TNT7	Q9QV9	OS Rattus norvegicus (Rat).
7	1774	61.3	539	2	Q70854	Q9QV9	OC Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
8	1774	61.3	539	2	CAE81922	Q9QV9	CC -I - SIMILARITY: Belongs to the amiloride-sensitive sodium channel family.
9	1671.5	57.8	558	2	Q70853	Q9QV9	DR EMBL; AU242554; CAB68361; -.
10	1671.5	57.8	558	2	CAE81923	Q9QV9	DR GO; GO:0005216; F:ion channel activity; IFA.
11	1473	50.9	417	2	Q6PIN9	Q9QV9	DR GO; GO:0005212; F:ion channel activity; IFA.
12	1473	50.9	417	2	Q70852	Q9QV9	DR GO; GO:0006811; F:ion transport; IEA.
13	1327	45.9	559	2	Q91YB8	Q91YB8	DR GO; GO:0006812; F:ion transport; IEA.
14	1318	45.6	296	2	Q6GMS1	Q91YB8	DR GO; GO:0006813; F:ion transport; IEA.
15	1296	44.8	2	Q88762	Q88762	DR GO; GO:0006814; F:ion transport; IEA.	
16	1275	44.1	526	1	BNA2_RAT	P5526	DR InterPro; IPR01873; Na+channel_ASC.
17	1274	44.1	526	2	Q6NKK8	Q6NKK8	DR Pfam; PF00858; ASC; 1.
18	1274	44.1	526	2	AAH67025	AAH67025	DR PRINT; PRO1078; AMIN CHANNEL.
19	1244.5	43.0	522	2	Q7TNT4	Q7TNT4	DR KW Ion transport; IONIC CHANNEL; Transmembrane; KW Transport.
20	1237.5	42.8	557	2	Q70858	Q70858	DR SEQUENCE ; 539 AA; 59352 MW; 2DE4838AA0547097 CRC64;
21	1237.5	42.8	557	2	QAE81918	QAE81918	DR Query Match Similarity 99.9%; Score 2889; DB 2; Length 539; Best Local Similarity 99.8%; Pred. No. 2, 6e-23; 0; Mismatches 38; Conservative Matches 38; Gap 0; Indels 0; Gaps 0
22	1236	42.7	574	1	BNA2_HUMAN	P78348	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
23	1232	42.6	529	2	Q70856	Q70856	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
24	1232	42.6	529	2	CAE81920	CAE81920	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
25	1198	41.4	533	2	Q53240	Q53240	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
26	1181	40.8	512	1	BNA1_MOUSE	Q923h0	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
27	1179	40.8	512	1	BNA1_MOUSE	Q923h0	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
28	1179	40.8	512	1	BNA1_RAT	Q92362	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
29	1171.5	40.5	501	2	Q70857	Q70857	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
30	1171.5	40.5	501	2	CAE81919	CAE81919	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
31	1170	40.5	531	2	Q75906	Q75906	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539

32 1165.5 40.3 531 2 Q9QV98 Quercus homo sapien  
33 1165.5 40.3 549 2 Q9QV93 Quercus3 homo sapien  
34 1165 40.3 543 2 Q9QV94 Quercus4 homo sapien  
35 1160 40.1 542 2 Q7TNT4 Quercus14 opsanus tau  
36 1142.5 39.5 532 2 Q6D63 Quercus263 homo sapien  
37 1132.5 39.2 563 2 Q61203 Quercus1513 ratius norv  
38 1129.5 39.1 533 2 Q70855 Quercus1203 mus musculus  
39 1128.5 39.0 533 2 QAE81921 Quercus1855 brachydantio  
40 1128.5 39.0 533 2 QAE81921 Quercus1921 brachydantion  
41 1117.5 38.6 563 2 Q8NJE2 Quercus32 homo sapien  
42 1109.5 38.4 533 2 Q7TNT3 Quercus113 opsanus tau  
43 1093 37.4 425 2 Q9QV91 Quercus1657 fugu rubripinnis  
44 951 32.9 309 2 Q7657 Quercus657 homo sapien  
45 840.5 29.1 344 2 Q96CV2 Quercus657 homo sapien

ALIGNMENTS

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2889	99.9	539	2	Q9QV9	Q9QV9	RESULT 1
2	2883	99.7	539	2	Q0JHS6	Q9QV9	PRELIMINARY; PRT; 539 AA.
3	2855	99.1	539	2	Q7TN7	Q9QV9;	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
4	2811	97.2	539	2	Q9NQ4	Q9NQ4	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
5	2787	96.4	524	2	Q80XK4	Q80XK4	DB SPASIC protein.
6	2680	92.7	647	2	Q7TNT7	Q9QV9	GN Name=Spasic;
7	1774	61.3	539	2	Q70854	Q9QV9	OS Rattus norvegicus (Rat).
8	1774	61.3	539	2	CAE81922	Q9QV9	OC Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
9	1671.5	57.8	558	2	Q70853	Q9QV9	CC -I - SIMILARITY: Belongs to the amiloride-sensitive sodium channel family.
10	1671.5	57.8	558	2	CAE81923	Q9QV9	DR EMBL; AU242554; CAB68361; -.
11	1473	50.9	417	2	Q6PIN9	Q9QV9	DR GO; GO:0005216; F:ion channel activity; IFA.
12	1473	50.9	417	2	Q70852	Q9QV9	DR GO; GO:0005212; F:ion channel activity; IFA.
13	1327	45.9	559	2	Q91YB8	Q91YB8	DR GO; GO:0006811; F:ion transport; IEA.
14	1318	45.6	296	2	Q6GMS1	Q6GMS1	DR GO; GO:0006812; F:ion transport; IEA.
15	1296	44.8	2	Q88762	Q88762	DR GO; GO:0006813; F:ion transport; IEA.	
16	1275	44.1	526	1	BNA2_RAT	P5526	DR InterPro; IPR01873; Na+channel_ASC.
17	1274	44.1	526	2	Q6NKK8	Q6NKK8	DR Pfam; PF00858; ASC; 1.
18	1274	44.1	526	2	AAH67025	AAH67025	DR PRINT; PRO1078; AMIN CHANNEL.
19	1244.5	43.0	522	2	Q7TNT4	Q7TNT4	DR KW Ion transport; IONIC CHANNEL; Transmembrane; KW Transport.
20	1237.5	42.8	557	2	Q70858	Q70858	DR SEQUENCE ; 539 AA; 59352 MW; 2DE4838AA0547097 CRC64;
21	1237.5	42.8	557	2	QAE81918	QAE81918	DR Query Match Similarity 99.9%; Score 2889; DB 2; Length 539; Best Local Similarity 99.8%; Pred. No. 2, 6e-23; 0; Mismatches 38; Conservative Matches 38; Gap 0; Indels 0; Gaps 0
22	1236	42.7	574	1	BNA2_HUMAN	P78348	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
23	1232	42.6	529	2	Q70856	Q70856	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
24	1232	42.6	529	2	CAE81920	CAE81920	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
25	1198	41.4	533	2	Q53240	Q53240	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
26	1181	40.8	512	1	BNA1_MOUSE	Q923h0	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
27	1179	40.8	512	1	BNA1_MOUSE	Q923h0	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
28	1179	40.8	512	1	BNA1_RAT	Q92362	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
29	1171.5	40.5	501	2	Q70857	Q70857	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
30	1171.5	40.5	501	2	CAE81919	CAE81919	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539
31	1170	40.5	531	2	Q75906	Q75906	DR 1 MPIEVCKIKFABEDARKPKE . . . . . LPNHHHHPHGPPGSLFENFAC 539

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On protein - protein search, using sw model

Run on: December 21, 2004, 09:47:03 ; Search time 23 Seconds  
(without alignments)  
2254.819 Million cell updates/sec

Title: US-09-701-747a-2  
Perfect score: 2892

Sequence: 1 MPIEIVCKIKPAAEDAKPKE.....LPNNHHPHGPPGSURENFA 539

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries.

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Length DB ID

#### Description

RESULT 1  
JE0091

testis sodium channel 1 - human

C.Species: Homo sapiens (man)

C.Date: 14-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004

C.Accession: JE0091

R.Ishibashi, K.; Maruno, F.

Biochem. Biophys. Res. Commun. 245, 589-593, 1998

A.Title: Molecular cloning of a DEGENAC sodium channel cDNA from human testis.

A.Reference number: JE0091; MUID:98238605; PMID:9571199

A.Accession: JE0091

A.Molecule type: mRNA

A.Residues: 1-532 <ISP>

A,Cross-references: UNIPROT:0606263; DDBJ:AB010575; NID:93097313; PIDN:BA25897.1; PID:9:

A.Experimental source: testis

C.Keywords: glycoprotein; mitochondrion

P:43-61;43-462/Region: hydrophobic

F:175/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.5%; Score 1142.5; DB 2; Length 532;

Best Local Similarity 45.9%; Pred. No. 2, 3.3e-85; DB Matches 247; Conservative 62; Mismatches 172; Indels 57; Gaps 12;

QY 35 GRPAPR---DLATFASSTLHGIGRACGPGPGLRLLTSLAAFLYQASLAR 90

Db 6 GPSEARROASDRDVFASCSMIGLIGHVFGPSLSLRGGWWAAKVVAVSVATEFLYQAVRR 65

QY 91 GYLTRPHVAMPAPAAPAVAGPAPVTLINIRFRHSAISDADIFHLAN--LTLGLPPKRD 148

Db 66 YYRBFHHTQALDBERHSHRLI-FPAVTLINPLRRLSRLTPNDL-HWAGSALLGDPREHA 123

QY 149 GHRAGKRYPEP-----DMDLILRTGQHLDAMLSKCNFGHGHICASNSFVWVTRY 199

Db 124 APLRALGRPAPPGFMPSPPTFQMAQLYARAGHSIDMDLIDCRFGPGCPGPEFTTIPTRM 183

QY 200 GKCYTFN---ADPOSSLPSRAGWGSGLIMLIDQOEWYLPWRETNNTSFEAGIRVQHHS 257

QY 184 GKTYTFNSGADGABLLTTRGGANGNGIDIMLDVQSBYLWVDRNEETPPEGIRVQH 243

Db 258 QEPQPYTHQLGFCGVSPQFQTYVSKCQDRLTYLPQPGMCNCRAS-----K 301

QY 244 HESRPIDDOLGLGQVSPGYQTYFVSCQDQLSFLPPNGDCCSASLNPNYEPSPSDPLGSPK 303

QY 302 LRPBPELOGISAYSVAECKLRCERKEAVIQRCHGVMVHMPGENETICPPNVIKEGADHDSL 361

Db 304 PPAPL---PFPFMGLLACTEYVARKCGMVMVPGDVYPCSPQYKNCAPADAM 359

QY 362 GGGSGPFCPTCNLTYTRGKISMVKPNRSARYLARKNNETYIRENPLVDFPE 421

Db 360 -LKDSDSACPNCACSTYKAKELSMRIPSPRARARFLARKTRREAYIAENVALLIF 417

QY 422 ALTSEAMEQRAAVGSLALGQGQMLPIGASILTLRILDYIVEVSMWDR-LKRVWRP 480

#### ALIGNMENTS

30 269.5 9.3 611 2 T20501 hypothetical prote  
31 264 9.1 978 2 T16948 hypothetical prote  
32 235.5 8.2 297 2 T25652 degenerin 1 (DEG-1)  
33 230 8.0 599 2 T15552 hypothetical prote  
34 229.5 7.9 907 2 T27317 hypothetical prote  
35 203 7.0 292 T29233 aniloxide-sensitivity  
36 190.5 6.6 606 2 JN0054 hypothetical prote  
37 160 5.5 384 2 T19513 hypothetical prote  
38 154.5 5.3 840 2 T21333 190K DNA-binding protein  
39 113 3.9 1596 2 A35927 transcription core  
40 110.5 3.8 1495 2 S60255 probable phosphotyrosine kinase  
41 104.5 3.6 956 2 B83200 polyketide synthase  
42 104.5 3.6 6260 2 T30228 peroxidasin - fruit  
43 103 3.6 1535 2 S46224 epidermal growth factor  
44 101.5 3.5 1207 1 EGHU protein-tyrosine kinase

GenCore version 5.1.6  
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OM protein - protein search, using SW model  
 Run on: December 21, 2004, 07:56:27 ; Search time 73 Seconds  
 (without alignments)

2648.700 Million cell updates/sec

Title: US-09-701-747A-2  
 Perfect score: 2892  
 Sequence: 1 MPIEVCKIKFKAEDAKPKR. . . . . LPNHHHHPGPPGSLPENFAC 539

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 200273

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: geneseq2008b:\*

2: geneseq1990b:\*

3: geneseq2008b:\*

4: geneseq2001b:\*

5: geneseq2004b:\*

6: geneseq2003a:\*

7: geneseq2003b:\*

8: geneseq2004b:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	RESULT 1
1	2892	100.0	539	3 AAY33870	AAV53870
2	2814	97.3	539	4 AAE10898	AAV53870 standard; protein: 539 AA.
3	2811	97.2	539	2 AAW80318	XX
4	2811	97.2	539	4 AAE10897	XX
5	2811	97.2	539	6 ABP8577	XX
6	2811	97.2	539	7 ADN38972	XX
7	2811	97.2	653	5 ABP63359	XX
8	2799	96.8	539	2 AAW80315	XX
9	2571	88.9	587	2 AAW80316	XX
10	1897	65.6	401	3 AAB07750	XX
11	1323	45.7	559	2 AAW8507	XX
12	1323	45.7	559	3 AAY6178	XX
13	1311.5	45.3	6	ABP0739	XX
14	1296	44.8	513	2 AAY03186	XX
15	1275	44.1	526	2 AAW8504	XX
16	1275	44.1	526	3 AAY6175	XX
17	1275	44.1	526	3 AAY6175	XX
18	1265	43.7	318	8 ADH22534	XX
19	1261	43.6	514	8 ADN61835	XX
20	1261	43.6	514	2 AAW8505	XX
21	1249.5	43.2	514	3 AAY6176	XX
22	1249.5	43.2	514	3 AAY6176	XX
23	1198	41.4	533	2 AAW8508	XX
24	1198	41.4	533	3 AAY6179	XX
25	1198	41.4	533	AAU10906	XX

#### ALIGNMENTS

26	1198	41.4	533	8 ADN97426	Adn97426 Rat DRASIC
27	1179	40.8	512	2 AAW68506	AAW68506 Human aci
28	1179	40.8	512	2 AAW93420	AAW93420 Human BNC
29	1179	40.8	512	3 AAY69177	Aay69177 A human aci
30	1179	40.8	512	5 AAU10905	Aau10905 Rat acid
31	1179	40.8	512	5 AAU10903	Aau10903 Human aci
32	1179	40.8	512	7 ADD14073	Add14073 Human src
33	1179	40.8	512	8 ADK7115	Adk7115 Human aci
34	1179	40.8	512	8 ADN97420	Adn97420 Rat BNCL
35	1179	40.8	512	8 ADP43821	Adp43821 Human aci
36	1179	40.5	531	2 AAY09509	Aay09509 Human pro
37	1179	40.5	531	8 AAU10904	Aau10904 Human aci
38	1170	40.5	531	8 ADN97424	Adn97424 Human DRA
39	1165.5	40.3	529	8 ADG28595	Adg28595 Human SIN
40	1165.5	40.3	531	3 AAY69181	Aay69181 A human aci
41	1165.5	40.3	531	7 AAE38601	Aae38601 Human aci
42	1165.5	40.3	531	7 ADP40465	Adp40465 Human aci
43	1165.5	40.3	549	2 AAW88252	AAW88252 Sodium ch
44	1165	40.3	543	2 AAW88250	AAW88250 Sodium ch
45	1139.5	39.4	518	2 AAW88251	AAW88251 Sodium ch

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: geneseq2008b:\*

2: geneseq1990b:\*

3: geneseq2008b:\*

4: geneseq2001b:\*

5: geneseq2004b:\*

6: geneseq2003a:\*

7: geneseq2003b:\*

8: geneseq2004b:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1

ID AAV53870

XX AAV53870;

XX AAV53870;

XX DT 13-MAR-2000 (first entry)

XX DE Amino acid sequence of a H+-gated cation channel designated SPASIC.

XX H+-gated cation channel; SPASIC; dorsal root ganglion; gene therapy; acid sensitive cation channel; central nervous system; pain response; ion channel activity; neurotransmitter release; analgesic; neurodegenerative; anti-inflammatory; neurotransmitter release; neuronal excitability.

XX OS Rattus norvegicus.

XX PN W09963181-A2.

XX PD 09-DEC-1999.

XX PF 03-JUN-1999; 99WO-GB001743.

XX PR 03-JUN-1998; 98GB-00011965.

XX PA (UNLO ) UNIV COLLEGE LONDON.

XX PI Wood JN, England S, Chen CC, Akopian AN;

XX DR WPI; 2000-086977/07.

XX N-PSDB; AA236802.

XX PT Novel ion channel protein for use as an analgesic drug target and for identifying novel analgesic and antiinflammatory agents.

XX Claim 2; Page 51-52, 55pp; English.

CC The Present sequence represents a H+-gated cation channel, designated SPASIC. The cDNA sequence was isolated from a rat dorsal root ganglion cDNA library. The protein is an acid sensitive cation channel capable of reversibly mediating rapid and sustained cation current. The channel is present in dorsal root ganglion and in central nervous system tissues. The SPASIC polynucleotide and polypeptide are used in influencing electrophysiological and/or pharmacological properties of a cell.

CC Expression of the SPASIC gene or antisense sequences leads to an increase or reduction in ion channel activity. The SPASIC gene is used in gene therapy or in preparation of medicaments for gene therapy to inhibit pain.

CC Aay69178 A rat aci

CC Abp69359 Human pro

CC Aaw80315 Neurodege

CC Aaw80316 Neurodege

CC Aab07750 A human a

CC Aaw68507 Rat acid

CC Aay69178 A rat aci

CC Abp70739 Human pro

CC Aay03185 Rat Acid

CC Aav68504 Rat Acid

CC Aav03188 Rat Acid

CC Aay69175 A rat aci

CC Adh22534 Human pro

CC Abp65092 Human Nov

CC Adb61835 Human nov

CC Aav68505 Human aci

CC Aay69176 A partial

CC Aaw68508 Rat acid

CC Aay69179 A rat aci

CC Aav10906 Rat acid

14	29	1.1	396	10	US-09-814-353-4322	Sequence 4322, App
15	29	1.1	395	15	US-10-212-677-20	Sequence 1056, A
15	29	1.1	396	15	US-10-361-811-20	Sequence 20, App
15	29	1.1	396	15	US-10-369-186-20	Sequence 20, App
17	29	1.1	451	9	US-09-860-670-39	Sequence 39, App
18	29	1.1	451	15	US-10-227-646-39	Sequence 39, App
19	29	1.1	462	15	US-10-101-510-176	Sequence 176, App
20	29	1.1	462	15	US-10-101-510-616	Sequence 616, App
21	29	1.1	574	9	US-09-919-580-71	Sequence 71, App
22	29	1.1	613	11	US-09-969-034-828	Sequence 828, App
23	29	1.1	891	14	US-10-198-814-1156	Sequence 6156, App
24	29	1.1	1374	17	US-10-437-963-84556	Sequence 8456, A
25	29	1.1	1654	18	US-10-425-115-4120	Sequence 44120, A
26	29	1.1	1654	19	US-10-425-115-4120	Sequence 44120, A
27	29	1.1	39	15	US-10-211-195-29	Sequence 28, App
28	29	1.1	39	15	US-10-219-195-34	Sequence 29, App
29	29	1.1	39	15	US-10-219-195-34	Sequence 34, App
30	29	1.1	39	15	US-10-219-195-34	Sequence 49, App
31	28	1.1	41	11	US-09-876-143-867	Sequence 867, App
32	28	1.1	46	9	US-09-827-219-22	Sequence 22, App
33	28	1.1	46	9	US-09-827-219-22	Sequence 22, App
34	28	1.1	62	16	US-10-182-377-182	Sequence 26, App
35	28	1.1	64	9	US-09-913-965-42	Sequence 182, App
36	28	1.1	67	9	US-09-933-965-245	Sequence 42, App
37	28	1.1	70	9	US-09-925-218-396	Sequence 245, App
38	28	1.1	70	14	US-10-102-806-96	Sequence 396, App
39	28	1.1	75	11	US-09-876-549-2069	Sequence 2069, App
40	28	1.1	75	14	US-10-102-806-96	Sequence 2069, App
41	28	1.1	75	17	US-10-102-806-96	Sequence 2069, App
42	28	1.1	78	14	US-10-102-806-96	Sequence 2069, App
43	28	1.1	93	14	US-10-102-806-96	Sequence 2069, App
44	28	1.0	93	14	US-10-102-806-96	Sequence 2069, App
45	28	1.0	93	14	US-10-102-806-96	Sequence 2069, App
46	28	1.0	93	14	US-10-102-806-96	Sequence 2069, App
47	28	1.0	93	14	US-10-102-806-96	Sequence 2069, App
48	28	1.0	93	14	US-10-102-806-96	Sequence 2069, App
49	28	1.0	93	14	US-10-102-806-96	Sequence 2069, App
50	28	1.0	93	14	US-10-102-806-96	Sequence 2069, App
51	28	1.0	93	14	US-10-102-806-96	Sequence 2069, App
52	28	1.0	93	14	US-10-102-806-96	Sequence 2069, App
53	28	1.0	93	14	US-10-102-806-96	Sequence 2069, App
54	28	1.0	93	14	US-10-102-806-96	Sequence 2069, App
55	28	1.1	107	14	US-09-923-035-3235	Sequence 3235, App
56	28	1.1	107	15	US-10-102-552-1055	Sequence 1055, App
57	28	1.1	108	9	US-09-823-011-6	Sequence 6, App
58	28	1.1	109	9	US-09-960-352-2566	Sequence 2566, App
59	28	1.1	110	10	US-09-746-783-195	Sequence 195, App
60	28	1.1	110	16	US-10-242-535A-45147	Sequence 45147, A
61	28	1.1	110	16	US-10-085-783A-45147	Sequence 45147, A
62	28	1.1	117	14	US-10-060-036-2150	Sequence 2750, App
63	28	1.1	118	16	US-10-242-535A-16946	Sequence 16946, A
64	28	1.1	118	16	US-10-085-783A-16946	Sequence 16946, A
65	28	1.1	119	15	US-10-102-552-429	Sequence 229, App
66	28	1.1	120	9	US-09-974-300-3749	Sequence 3749, App
67	28	1.1	121	9	US-09-983-962-3235	Sequence 4235, App
68	28	1.1	122	9	US-09-878-178-1190	Sequence 1190, App
69	28	1.1	122	13	US-10-046-935-1190	Sequence 1190, App
70	28	1.1	122	14	US-10-091-483-279	Sequence 1190, App
71	28	1.1	123	15	US-10-102-552-4290	Sequence 240, App
72	28	1.1	130	9	US-09-764-846-379	Sequence 279, App
73	28	1.1	130	9	US-09-764-846-379	Sequence 279, App
74	28	1.1	130	10	US-09-764-846-379	Sequence 343, App
75	28	1.1	130	10	US-09-764-846-379	Sequence 343, App
76	28	1.1	130	10	US-09-764-846-379	Sequence 343, App
77	28	1.1	130	14	US-10-091-483-279	Sequence 279, App
78	28	1.1	130	14	US-10-091-483-343	Sequence 343, App
79	28	1.1	130	15	US-10-102-552-4290	Sequence 240, App
80	28	1.1	130	15	US-10-242-535A-16946	Sequence 16946, A
81	28	1.1	131	9	US-09-864-864-164	Sequence 164, App
82	28	1.1	133	16	US-10-242-535B-51549	Sequence 51549, A
83	28	1.1	133	16	US-10-005-783A-51549	Sequence 51549, A
84	28	1.1	133	16	US-10-005-783A-51549	Sequence 51549, A

Sequence 11864, A	Sequence 11888, A
Sequence 11944, A	Sequence 11949, A
Sequence 11949, A	Sequence 12015, A
Sequence 12015, A	Sequence 12088, A
Sequence 12088, A	Sequence 12103, A
Sequence 12103, A	Sequence 12127, A
Sequence 12127, A	Sequence 12131, A
Sequence 12131, A	Sequence 12137, A
Sequence 12137, A	Sequence 12322, A
Sequence 12322, A	Sequence 12368, A
Sequence 12368, A	Sequence 13499, A
Sequence 13499, A	Sequence 13556, A
Sequence 13556, A	Sequence 12087, A
Sequence 12087, A	Sequence 12175, A
Sequence 12175, A	Sequence 12195, A
Sequence 12195, A	Sequence 12429, A
Sequence 12429, A	Sequence 12450, A
Sequence 12450, A	Sequence 11710, A
Sequence 11710, A	Sequence 2, Appli
Sequence 2, Appli	Sequence 12161, A
Sequence 12161, A	Sequence 1174, A
Sequence 1174, A	Sequence 13820, A
Sequence 13820, A	Sequence 12079, A
Sequence 12079, A	Sequence 12350, A
Sequence 12350, A	Sequence 59, Appli
Sequence 59, Appli	Sequence 8100, A
Sequence 8100, A	Sequence 8863, A
Sequence 8863, A	Sequence 8942, A
Sequence 8942, A	Sequence 7801, A
Sequence 7801, A	Sequence 8044, A
Sequence 8044, A	Sequence 7751, A
Sequence 7751, A	Sequence 18058, A
Sequence 18058, A	Sequence 7748, A
Sequence 7748, A	Sequence 8623, A
Sequence 8623, A	Sequence 8655, A
Sequence 8655, A	Sequence 18071, A
Sequence 18071, A	Sequence 18058, A
Sequence 18058, A	Sequence 8070, A
Sequence 8070, A	Sequence 16234, A
Sequence 16234, A	Sequence 60, Appli
Sequence 60, Appli	Sequence 1912, A
Sequence 1912, A	Sequence 63, Appli
Sequence 63, Appli	Sequence 8073, A
Sequence 8073, A	Sequence 18062, A
Sequence 18062, A	Sequence 18062, A
Sequence 18062, A	Sequence 16, Appli
Sequence 16, Appli	Sequence 64, Appli
Sequence 64, Appli	Sequence 13636, A
Sequence 13636, A	Sequence 13, Appli
Sequence 13, Appli	Sequence 1233, A
Sequence 1233, A	Sequence 12220, A
Sequence 12220, A	Sequence 1585, A
Sequence 1585, A	Sequence 17945, A
Sequence 17945, A	Sequence 24, Appli
Sequence 24, Appli	Sequence 28, Appli
Sequence 28, Appli	Sequence 28, Appli
Sequence 28, Appli	Sequence 484, A
Sequence 484, A	Sequence 1701, A
Sequence 1701, A	Sequence 1701, A
Sequence 1701, A	Sequence 124, A
Sequence 124, A	Sequence 17039, A
Sequence 17039, A	Sequence 1322, A
Sequence 1322, A	Sequence 29, Appli
Sequence 29, Appli	Sequence 29, Appli
Sequence 29, Appli	Sequence 17067, A
Sequence 17067, A	Sequence 1455, A

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Om nucleic - nucleic search, using sw model

Run on: December 21, 2004, 03:54:47 ; Search time 5273 Seconds  
 (without alignments)  
 18119.662 Million cell updates/sec

Title: US-09-701-747a-1

Perfect score: 2622

Sequence: 1 agtgacagatgtggggc.....aaaaaaaaaaaaaa 2622

Scoring table: OLIGO-NUC

Gapext 60.0 , Gapext 60.0.

Searched: 32822875 seqs, 18219865908 residues

Word size : 16

Total number of hits satisfying chosen parameters: 2484663

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database : EST+\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_htc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gs81:\*

9: gb\_gs82:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	430	16.4	464	2 BPF55208
2	323	12.3	405	6 CB810840
3	309	11.8	391	6 CB75482
4	302	11.5	384	6 CB703338
5	299	11.4	435	6 CB792852
6	187	6.5	451	6 CB787201
7	170	6.5	473	6 CB730080
8	161	6.1	799	6 CA149777
9	156	5.9	480	8 BZ275617
10	152	5.8	690	5 BUT09210
11	152	5.8	825	4 BII31397
12	128	4.9	633	5 BU058742
13	128	4.9	724	5 BQ42411
14	127	4.8	658	2 BB621654
15	123	4.7	426	5 BY295044
16	86	3.3	400	1 AL362900
17	86	3.3	730	8 A2Z79355
18	82	3.1	719	8 A2Z70766
19	81	3.1	451	5 BY290885
20	80	3.1	779	5 BX35391
21	78	3.0	816	9 CR220242
C	22	2.7	323	2 AW530335
C	23	2.7	337	7 CR47643
C	24	2.7	400	2 BP393596

97	C	25	72	2.7	473	2	BR411609
	C	26	72	2.7	474	2	AW527475
	C	27	72	2.7	703	4	BW386997
	C	28	72	2.7	712	8	BZ195341
	C	29	70	2.7	512	2	BEI21355
	C	30	68	2.6	516	4	BG913294
	C	31	66	2.5	450	6	CA451772
	C	32	66	2.5	585	6	CB058292
	C	33	60	2.3	616	4	BG912088
	C	34	52	2.0	130	4	BB595752
	C	35	44	1.7	740	4	BG911389
	C	36	41	1.6	1150	2	BPF31115
	C	37	37	1.4	678	2	BB620134
	C	38	37	1.4	833	9	CR271533
	C	39	36	1.4	528	6	CB452403
	C	40	36	1.4	528	6	CB465468
	C	41	35	1.3	206	2	BB27030
	C	42	35	1.3	210	2	BB382859
	C	43	35	1.3	213	2	BB418210
	C	44	35	1.3	220	2	BB35928
	C	45	35	1.3	241	2	BB607280
	C	46	35	1.3	274	2	BX638893
	C	47	35	1.3	275	2	BB027741
	C	48	35	1.3	368	4	BY1731176
	C	49	35	1.3	382	6	BY656489
	C	50	35	1.3	433	6	BYX5280
	C	51	35	1.3	679	1	AV323885
	C	52	35	1.3	759	1	AQ353117
	C	53	33	1.3	423	2	AW669129
	C	54	33	1.3	1019	9	CNS01070
	C	55	32	1.2	304	6	CA335120
	C	56	32	1.2	327	2	AM345756
	C	57	31	1.2	272	2	BB421805
	C	58	31	1.2	359	6	CD773159
	C	59	31	1.2	369	4	BH531723
	C	60	31	1.2	397	4	BH531320
	C	61	31	1.2	479	7	BU173697
	C	62	31	1.2	483	6	CA779219
	C	63	31	1.2	708	4	BG313866
	C	64	31	1.2	722	6	CB320076
	C	65	31	1.2	846	7	CN154737
	C	66	31	1.2	1101	9	CNS00E01
	C	67	31	1.2	1116	2	BPF527059
	C	68	30	1.2	132	2	AW068845
	C	69	30	1.1	132	2	AW068845
	C	70	30	1.1	136	6	CA337176
	C	71	30	1.1	146	5	BU962336
	C	72	30	1.1	167	6	CA67348
	C	73	30	1.1	205	4	BM570366
	C	74	30	1.1	219	5	BB587065
	C	75	30	1.1	237	5	BW638385
	C	76	30	1.1	268	4	BU1703515
	C	77	30	1.1	290	7	CPT74275
	C	78	30	1.1	292	7	CO417007
	C	79	30	1.1	296	7	AM360147
	C	80	30	1.1	316	7	CK375527
	C	81	30	1.1	320	7	CK402038
	C	82	30	1.1	335	7	CN995507
	C	83	30	1.1	373	4	BM919322
	C	84	30	1.1	384	7	CNU42061
	C	85	30	1.1	385	5	BN965797
	C	86	30	1.1	443	2	AW734179
	C	87	30	1.1	489	5	BQ284601
	C	88	30	1.1	528	7	CK983788
	C	89	30	1.1	559	7	CO947777
	C	90	30	1.1	561	7	CRK73206
	C	91	30	1.1	730	6	CA821549
	C	92	30	1.1	804	1	AL666096
	C	93	30	1.1	804	9	AG516356
	C	94	30	1.1	988	9	CB197997
	C	95	30	1.1	1005	5	BQ790397
	C	96	30	1.1	1013	5	BU178304
	C	97	30	1.1	1013	5	CRP245533

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OM nucleic - nucleic search, using sw model  
Run on: December 21, 2004, 02:00:56 ; Search time 818 Seconds  
Sequence: 1 agtgacagctgtgcgggtgc.....aaaaaaaaaaaaaaaa 2622

Title: US-09-701-747A-1  
Perfect score: 2622  
Scoring table: OLIGO-NUC  
Gapop-60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues  
Word size : 16  
Total number of hits satisfying chosen parameters: 249225  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: listing first 500 summaries  
Database : N\_Geneseq\_23Sep04:  
1: geneseqn1980s: \*  
2: geneseqn1990s: \*  
3: geneseqn2000s: \*  
4: geneseqn2001as: \*  
5: geneseqn2001bs: \*  
6: geneseqn2002ab: \*  
7: geneseqn2002bs: \*  
8: geneseqn2003ab: \*  
9: geneseqn2003bs: \*  
10: geneseqn2004ab: \*  
11: geneseqn2004bs: \*  
12: geneseqn2004bs: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2622	100.0	2622 3 AAZ36802	Aaz36802 Nucleic acid
2	80	3.1	2431 6 ABD211576	Ab211576 Human pol
3	80	3.1	2431 12 ADM44094	Adm44094 Novel human
4	80	3.1	2516 3 AAS5323	Aas5323 DNA encod
5	80	3.1	2528 5 AAD18265	Aad18265 Human bra
6	80	3.1	2710 10 ACR72703	Accr72703 Human can
7	80	3.1	2710 11 ADN38971	Adn38971 Cancer/an
8	80	3.1	2711 2 AAV68056	Aav68056 Neurodege
9	80	3.1	2752 12 AHD22600	Ahd22600 CDNA enco
10	80	3.1	2955 2 AAV68057	Aav68057 Neurodege
11	68	2.6	462 9 ACH13269	Ach13269 Human adu
12	68	2.6	465 9 ACH1266	Ach1266 Human adu
13	68	2.6	1203 3 AAS5324	Aas5324 Coding re
14	68	2.6	1632 2 AAV68059	Aav68059 Neurodege
15	68	2.6	1633 2 ABD18260	Abd18260 Human bra
16	32	1.2	50 5 AAD18264	Aad18264 Oligo use
17	31	1.2	40 5 ABQ57925	Abq57925 Human col
18	30	1.1	424 6 AAI14984	Aai14984 Human bre
19	29	1.1	313 5 ABV04496	Abv04496 Human pro
20	29	1.1	335 5 ABV57836	Abv57836 Human pro
21	28	1.1	4 ABL97914	Ab197914 Human tes

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OM nucleic - nucleic search, using bw model

Run on:

December 21, 2004, 02:03:42 (without alignments)  
17154.620 Million cell updates/sec

Title: US-09-701-747a-1

Perfect score: 2622

Sequence: 1 agtgacagctgtgcgggtgc.....aaaaaaaaaaaaaaaaaa 2622

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext: 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 16

Total number of hits satisfying chosen parameters: 478857

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 500 summaries

Database : GenEmbl:\*

1: gb\_baa:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_p1:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vri:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	2622	100.0	2622	6	AX009297	AX009297 Sequence
2	2195	83.7	2622	10	RNO042554	AJ742554 Rattus no
3	1761	67.2	2532	10	RNO071642	AJ71642 Rattus no
4	823	31.4	216648	10	AC112361	AC112361 Rattus no
5	823	31.4	266167	2	AC121633	AC121633 Rattus no
6	161	6.1	2303	10	BC046481	BC046481 Mus muscu
7	6.1	6.1	2478	10	BC055772	BC055772 Mus muscu
8	137	5.2	177632	2	AC115011	AC114651 Mus muscu
9	137	5.2	197109	2	AC115011	AC115011 Mus muscu
10	80	3.1	744	9	HS405881	AJ408881 Homo sapi
11	80	3.1	2528	6	AR0306271	AR306271 Sequence
12	80	3.1	2509	9	BC010439	BC010439 Homo sapi
13	80	3.1	2711	6	E31843	E31843 Novel compo
14	80	3.1	2711	6	AX002412	AX002412 Sequence
15	80	3.1	2955	6	E31844	E31844 Novel compo
16	80	3.1	2955	6	AK002414	AX002414 Sequence
17	80	3.1	3345	9	BC031812	BC031812 Homo sapi
18	80	3.1	3345	9	AJ271643	AJ271643 Homo sapi
19	80	3.1	183625	9	AC053503	AC053503 Homo sapi

Score	Match	Length	DB	ID	Description	
20	80	3.1	184176	2	AC149120	AC149120 Papio anu
21	80	3.1	186883	2	AC00991	AC00991 Homo sapi
22	80	3.1	193054	2	AC149860	AC149860 Papio anu
23	68	2.6	1620	6	AR306270	AR306270 Sequence
24	68	2.6	1632	6	E31846	E31846 Novel compo
25	68	2.6	1632	6	AK02418	AK02418 Sequence
26	68	2.6	2439	9	BC073912	BC073912 Homo sapi
27	63	2.4	200465	2	AC148786	AC148786 Otolemur
28	63	2.4	215101	2	AC14887	AC14887 Otolemur
29	59	2.3	1452	6	CQ714799	CQ714799 Sequence
30	50	1.9	1315	9	HSA08882	HSA08882 Homo sapi
31	50	1.9	135033	9	AC09955	AC09955 Homo sapi
32	42	1.6	53239	2	AC011971	AC011971 Homo sapi
33	40	1.5	65	6	CQ532496	CQ532496 Sequence
34	32	1.2	50	6	AR306265	AR306265 Sequence
35	31	1.2	40	6	AR306269	AR306269 Sequence
36	30	1.1	601	11	G94636	G94636 S20816415RB
37	29	1.1	271	5	CQ422415	CQ422415 Sequence
38	29	1.1	313	6	AC042620	AC042620 Sequence
39	29	1.1	335	6	CQ525988	CQ525988 Sequence
40	29	1.1	396	6	CQ397251	CQ397251 Sequence
41	29	1.1	396	6	CQ403555	CQ403555 Sequence
42	29	1.1	396	6	AR91197	AR91197 Sequence
43	29	1.1	395	6	AR92902	AR92902 Sequence
44	29	1.1	396	6	AR89632	AR89632 Sequence
45	29	1.1	396	6	AR93873	AR93873 Sequence
46	29	1.1	227369	2	AC093202	AC093202 Sequence
47	29	1.1	230637	2	AX381133	AX381133 Sequence
48	29	1.1	1547	9	HSA08884	HSA08884 Homo sapi
49	29	1.1	183793	2	CR450793	CR450793 Homo sapi
50	29	1.1	186883	2	AC040991	AC040991 Homo sapi
51	29	1.1	190260	2	CR538726	CR538726 Danio rer
52	29	1.1	227369	2	AC114469	AC114469 Rattus no
53	29	1.1	230637	2	AC053345	AC053345 Rattus no
54	29	1.1	246991	2	AC122956	AC122956 Rattus no
55	29	1.1	249173	2	AC138856	AC138856 Rattus no
56	28	1.1	44	6	AR038858	AR038858 Sequence
57	28	1.1	46	6	AX207759	AX207759 Sequence
58	28	1.1	46	6	AX207583	AX207583 Sequence
59	28	1.1	51	6	CQ05099	CQ05099 Sequence
60	28	1.1	54	6	A49113	A49113 Sequence 8
61	28	1.1	55	6	AR420154	AR420154 Sequence
62	28	1.1	55	6	AX980848	AX980848 Sequence
63	28	1.1	55	6	BD115707	BD115707 EST and e
64	28	1.1	57	6	AK90358	AK90358 Sequence
65	28	1.1	57	6	AR209491	BD039491 Sequence
66	28	1.1	59	6	AR420379	AR420379 Sequence
67	28	1.1	59	6	AX981073	AX981073 Sequence
68	28	1.1	59	6	BD115932	BD115932 EST and e
69	28	1.1	62	6	AX205290	AX205290 Sequence
70	28	1.1	69	6	AR420390	AR420390 Sequence
71	28	1.1	69	6	AR420957	AR420957 Sequence
72	28	1.1	69	6	AX981084	AX981084 Sequence
73	28	1.1	69	6	AK911651	AK911651 Sequence
74	28	1.1	69	6	BD115943	BD115943 EST and e
75	28	1.1	69	6	BD116510	BD116510 EST and e
76	28	1.1	70	6	AR420943	AR420943 Sequence
77	28	1.1	70	6	AK981637	AK981637 Sequence
78	28	1.1	70	6	BD116496	BD116496 EST and e
79	28	1.1	72	6	AR420893	AR420893 Sequence
80	28	1.1	72	6	AK981587	AK981587 Sequence
81	28	1.1	72	6	BD116446	BD116446 EST and e
82	28	1.1	73	6	AR423201	AR423201 Sequence
83	28	1.1	73	6	AK983895	AK983895 Sequence
84	28	1.1	73	6	BD118754	BD118754 EST and e
85	28	1.1	77	6	AR420769	AR420769 Sequence
86	28	1.1	77	6	AX981463	AX981463 Sequence
87	28	1.1	77	6	BD116322	BD116322 EST and e
88	28	1.1	81	6	AR119865	AR119865 Sequence
89	28	1.1	81	6	AR420701	AR420701 Sequence
90	28	1.1	81	6	AR422104	AR422104 Sequence
91	28	1.1	81	6	AX981395	AX981395 Sequence
92	28	1.1	81	6	AX982798	AX982798 Sequence



OM nucleic - nucleic search, using sw model  
Run on: December 20, 2004, 21:43:21 : Search time 151 Seconds  
(without alignment)  
Scoring table: IDENTITY\_NUC  
Sequence: 1 aggacacgtgtgggggc.....aaaaaaaaaaaaaaaaaaaa 2522  
Gapop 10.0 , Gapext 1.0  
Searched: 824507 seqs, 35539441 residues  
Total number of hits satisfying chosen parameters: 1649014  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1748	66.7	2528	4	US-09-318-959-7	Sequence 1, Appli
2	1717	65.5	2431	4	US-09-319-451-45B	Sequence 458, Appli
3	1400.8	53.4	1620	4	US-09-518-959-6	Sequence 6, Appli
4	491.2	18.7	3647	3	US-09-360-197-3	Sequence 7, Appli
5	440.2	16.8	1620	3	US-09-360-197-3	Sequence 3, Appli
6	415	15.8	3562	3	US-09-360-197-1	Sequence 1, Appli
7	391.2	14.9	1736	3	US-09-360-197-13	Sequence 13, Appli
8	351	13.4	1602	3	US-09-360-197-9	Sequence 9, Appli
9	347.2	13.2	1948	3	US-09-360-197-11	Sequence 11, Appli
10	335	12.8	1539	2	US-08-828-598-1	Sequence 1, Appli
11	335	12.8	1539	4	US-09-016-434-1102	Sequence 1102, Appli
12	335	12.8	1666	3	US-09-360-197-5	Sequence 5, Appli
13	173.6	6.6	393	4	US-09-016-434-206	Sequence 206, Appli
14	47.8	1.8	7218	1	US-08-222-463-14	Sequence 14, Appli
15	43.2	1.6	2218	2	US-08-845-998-5	Sequence 5, Appli
16	43.2	1.6	2218	3	US-09-006-537-5	Sequence 5, Appli
17	43.2	1.6	2218	3	US-09-430-854-5	Sequence 5, Appli
18	42.8	1.6	1605	4	US-09-449-476-187	Sequence 187, Appli
19	40.8	1.6	985	4	US-09-222-403-25	Sequence 25, Appli
20	40.8	1.6	985	4	US-09-222-403-27	Sequence 27, Appli
21	40.8	1.6	985	4	US-09-431-527-25	Sequence 25, Appli
22	40.8	1.6	985	4	US-09-431-527-27	Sequence 27, Appli
23	40.6	1.5	2639	3	US-09-374-135-1	Sequence 1, Appli
24	40.6	1.5	7218	1	US-08-222-463-14	Sequence 14, Appli
25	40.4	1.5	1988	2	US-08-712-948-8	Sequence 8, Appli
26	40.4	1.5	1988	4	US-09-023-655-1218	Sequence 1218, Appli
27	40.4	1.5	2259	2	US-08-845-998-3	Sequence 3, Appli

CATWALK

## ALIGNMENT

OM nucleic - nucleic search, using sw model  
Run on: December 20, 2004, 21:43:21 : Search time 151 Seconds  
(without alignment)  
Scoring table: IDENTITY\_NUC  
Sequence: 1 aggacacgtgtgggggc.....aaaaaaaaaaaaaaaaaaaa 2522  
Gapop 10.0 , Gapext 1.0  
Searched: 824507 seqs, 355394411 residues  
Total number of hits satisfying chosen parameters: 1649014  
Minimum DB seq length: 0  
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Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listeing first 45 summaries

Database : Issued Patents NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1748	66.7	2528	4	US-09-318-959-7	Sequence 1, Appli
2	1717	65.5	2431	4	US-09-319-945-45B	Sequence 458, Appli
3	1400.8	53.4	1620	4	US-09-518-959-6	Sequence 6, Appli
4	491.2	18.7	3647	3	US-09-360-197-3	Sequence 7, Appli
5	440.2	16.8	1620	3	US-09-360-197-3	Sequence 3, Appli
6	415	15.8	3562	3	US-09-360-197-1	Sequence 1, Appli
7	391.2	14.9	1736	3	US-09-360-197-13	Sequence 13, Appli
8	351	13.4	1602	3	US-09-360-197-9	Sequence 9, Appli
9	347.2	13.2	1948	3	US-09-360-197-11	Sequence 11, Appli
10	335	12.8	1539	2	US-08-828-598-1	Sequence 1, Appli
11	335	12.8	1539	4	US-09-016-434-1102	Sequence 1102, Appli
12	335	12.8	1666	3	US-09-360-197-5	Sequence 5, Appli
13	173.6	6.6	393	4	US-09-016-434-205	Sequence 206, Appli
14	47.8	1.8	7218	1	US-08-222-463-14	Sequence 14, Appli
15	43.2	1.6	2218	2	US-08-845-998-5	Sequence 5, Appli
16	43.2	1.6	2218	3	US-09-006-537-5	Sequence 5, Appli
17	43.2	1.6	2218	3	US-09-430-854-5	Sequence 5, Appli
18	42.8	1.6	1605	4	US-09-449-476-187	Sequence 187, Appli
19	40.8	1.6	985	4	US-09-222-405-25	Sequence 25, Appli
20	40.8	1.6	985	4	US-09-222-409-27	Sequence 27, Appli
21	40.8	1.6	985	4	US-09-431-527-25	Sequence 25, Appli
22	40.8	1.6	985	4	US-09-431-527-27	Sequence 27, Appli
23	40.6	1.5	2639	3	US-09-374-135-1	Sequence 1, Appli
24	40.6	1.5	7218	1	US-08-222-463-14	Sequence 14, Appli
25	40.4	1.5	1988	2	US-08-712-948-8	Sequence 8, Appli
26	40.4	1.5	1988	4	US-09-023-655-1218	Sequence 1218, Appli
27	40.4	1.5	2259	2	US-08-845-998-3	Sequence 3, Appli

RESULT 1	US-09-518-959-7
Sequence 7, Application US/09518959	
GENERAL INFORMATION:	
Patent No. 6548270	
APPLICANT: Dubin, Adrienne E	
APPLICANT: Erlander, Mark G	
APPLICANT: Huvar, Rene	
APPLICANT: Pyati, Jayashree	
TITLE OF INVENTION: DNA encoding human acid-sensing ion	
TITLE OF INVENTION: channel Brnac4 (ASIC4)	
FILE REFERENCE: ORT-1197	
CURRENT APPLICATION NUMBER: US/09/518,959	
CURRENT FILING DATE: 2000-03-03	
NUMBER OF SEQ ID NOS: 9	
SOFTWARE: PatentIn Ver. 2.1	
SEQ ID NO: 7	
LENGTH: 2528	
TYPE: DNA	
ORGANISM: Homo sapiens	
US-09-518-959-7	
Query Match Similarity 66.7%; Score 1748; DB 4; Length 2528;	
Best Local Similarity 84.1%;保守性 0; Mismatches 353; Indels 49; Gaps 13;	
Matches 2131; Conservative 0; Mismatches 353; Indels 49; Gaps 13;	
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DB 1 ACTCCCCACCTCGGCCGCCACCTGTCTGCTCTCCGCTGTGAGTTAG 60	
QY 188 AAGAGCAGCGCTGCCACCAACCACTCGGAGGGCACAGGGGTGCTCCAGGGAG 247	
DB 6 1 AAGAGCAGCGCTGCCACCACTCGGAGGGCACAGGGGTGCTCCAGGGAG 120	
QY 248 GACAGTAGCTGTGAGGCTCTGGCTGAGGGAGGAGGAGGAGGAGGAGGAT 307	
DB 121 GACAG-GGAGGGAGCTCTGGCTGAGGGAGGAGGAGGAGGAGGAGGAGGAT 179	
QY 308 GTGTCGAATCAATTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 367	
DB 180 GTGTCGAATCAATTGTGAGGAGGAGGAGGAGGAGGAGGAGGAT 239	
QY 368 GAGCAGAGCTCTGGGTGCTAGGGAGGAGGAGGAGGAGGAGGAGGAT 427	
DB 240 GAGCAGAGCTCTGGGTGCTAGGGAGGAGGAGGAGGAGGAGGAGGAT 399	
QY 428 GCCAGCAGCTGACTCTGTGAGGGCTGGCGGCCAGGCCCATGACTGT 487	
DB 300 GCGAGCAGCACCTGTGATGACTGGCGGCCGCTGTGGCCAGGCCACGACTG 359	





